10/575114

SEQUENCE LISTING AP20 Rec'd PCT/FTO 10 APR 2006

<110> KYOWA HAKKO KOGYO CO., LT	D
---------------------------------	---

<120> Ganglioside GM2-specific antibody composition

<130> 11622WO1

<150> P2003-350168 -

<151> 2003-10-09

<150> P2004-129431

<151> 2004-04-26

<160> 43

<170> PatentIn Ver. 2.1

<210> 1

<211> 1504

<212> DNA

<213> Cricetulus griseus

<220>

<221> CDS

<222> (1.)..(1119)

<400> 1

atg gct cac gct ccc gct agc tgc ccg agc tcc agg aac tct ggg gac

Met Ala His Ala Pro Ala Ser Cys Pro Ser Ser Arg Asn Ser Gly Asp

1 10 15

ggc gat aag ggc aag ccc agg aag gtg gcg ctc atc acg ggc atc acc 96 Gly Asp Lys Gly Lys Pro Arg Lys Val Ala Leu Ile Thr Gly Ile Thr

20 25 30

ggc cag gat ggc tca tac ttg gca gaa ttc ctg ctg gag aaa gga tac 144 Gly Gln Asp Gly Ser Tyr Leu Ala Glu Phe Leu Leu Glu Lys Gly Tyr Best Available Copy

_	_	His		_	_	_			Asn		 cga Arg	192
	Glu							Ile			atg Met 80	240
				Asp						-	atc Ile	288
			gtc Val 100									336
			att Ile									384
			acc Thr								ctt Leu ·	432
			gtg Val									480
			gaa Glu				•			Tyr		528
			gga Gly 180		Leu				Ile			576

,							Leu				aac Asn						624
•											gtt Val						672
											ctg Leu 235						720
											cat His						768
	-										gaa Glu						816
											gaa Glu					tca Ser	864
			•								gaa Glu						912
,											att Ile 315						960
	. –				-						ttc Phe						1008
	tcc	aag	gcg.	cag	cag	aaa	ctg	aac	tgg	aag	ccc	cgc	gtt	gcc	ttt	gac	1056

Ser Lys Ala Gln Gln Lys Leu Asn Trp Lys Pro Arg Val Ala Phe Asp 340 345 350 gag ctg gtg agg gag atg gtg caa gcc gat gtg gag ctc atg aga acc 1104 Glu Leu Val Arg Glu Met Val Gln Ala Asp Val Glu Leu Met Arg Thr 355 360 365 aac ccc aac gcc tga gcacctctac aaaaaaaattc gcgagacatg gactatggtg 1159 Asn Pro Asn Ala 370 cagagecage caaccagagt ccagecacte etgagaccat egaccataaa ecetegaetg 1219 cetgtgtegt ecceaeaget aagagetggg ceaeaggttt gtgggeaeea ggaeggggae 1279 actecagage taaggecact tegettttgt caaaggetee teteaatgat tttgggaaat 1339. caagaagttt aaaatcacat actcatttta cttgaaatta tgtcactaga caacttaaat 1399 ttttgagtet tgagattgtt tttetetttt ettattaaat gatettteta tgacceagea 1459 1504 <210> 2 <211> 372 <212> PRT <213> Cricetulus griseus <400>.2 Met Ala His Ala Pro Ala Ser Cys Pro Ser Ser Arg Asn Ser Gly Asp 1 5 10 15 Gly Asp Lys Gly Lys Pro Arg Lys Val Ala Leu Ile Thr Gly Ile Thr 20 25 30 Gly Gln Asp Gly Ser Tyr Leu Ala Glu Phe Leu Leu Glu Lys Gly Tyr 35 45 Glu Val His Gly Ile Val Arg Arg Ser Ser Ser Phe Asn Thr Gly Arg 50 55 60

Ile Glu His Leu Tyr Lys Asn Pro Gln Ala His Ile Glu Gly Asn Met

Lys	Leu	His	Tyr	Gly 85	Asp	Leu	Thr	Asp	Ser 90		Cys	Leu	Val	Lys 95	
Ile	Asn	Glu	Val 100		Pro	Thr	Glu	Ile 105		Asn	Leu	Gly	Ala 110		Ser
His	Val	Lys 115		Ser	· Phe	Asp	Leu 120	Ala	Glu	Tyr	Thr	Ala 125	_	Val	Asp
Gly	Val 130	Gly	Thr	Leu	Arg	Leu 135	Leu	Asp	Ala	Ile	Lys 140	Thr	Cys	Gly	Leu
Ile 145	Asn	Ser	Val	Lys	Phe 150	Tyr	Gln	Ala	Ser	Thr 155	Ser	Glu	Leu	Tyr	Gly 160
Lys	Val	Gln	Glu	Ile 165	Pro	Gln	Lys	Glu	Thr 170	Thr	Pro	Phe	Tyr	Pro 175	Arg
Ser	Pro	Tyr	Gly 180	Ala	Ala	Lys	Ĺeu	Tyr 185	Ala	Tyr	Tṛp	Ile	Val 190	Val	Asn
Phe	Arg	Glu 195	Ala	Tyr	Asn	Leu	Phe 200	Ala	Val	Asn	Gly	,Ile 205	Leu	Phe	Asn
His	Glu 210	Ser	Pro	Arg	Arg	Gly 215	Ala	Asn	Phe	Val	Thr 220	Arg	Lys	Ile	Ser
Arg 225	Ser	Val	Ala	Lys	Ile 230		Leu	Gly	Gln	Leu 235	Glu	Cys	Phe	Ser	Leu 240
Gly	Asn	Leu	Asp	Ala 245	Lys	Arg	Asp	Trp	Gly 250	His-	Ala	Lys	Asp.	Tyr 255	Val
Glu	Ala	Met	Trp 260	Leu	Met	Leu	Gln	Asn 265	Asp	Glu	Pro	Glu	Asp 270	Phe	Val

Ile Ala Thr Gly Glu Val His Ser Val Arg Glu Phe Val Glu Lys Ser 275 280 285

Phe Met His Ile Gly Lys Thr Ile Val Trp Glu Gly Lys Asn Glu Asn 290 295 300

Glu Val Gly Arg Cys Lys Glu Thr Gly Lys Ile His Val Thr Val Asp 305 310 315 320

Leu Lys Tyr Tyr Arg Pro Thr Glu Val Asp Phe Leu Gln Gly Asp Cys
325 330 335

Ser Lys Ala Gln Gln Lys Leu Asn Trp Lys Pro Arg Val Ala Phe Asp 340 345 350

Glu Leu Val Arg Glu Met Val Gln Ala Asp Val Glu Leu Met Arg Thr 355 360 365

Asn Pro Asn Ala 370

<210> 3

<211> 1316

<212> DNA

<213> Cricetulus griseus

. <400> 3

georececce etecacetg acceagagta getggagaat tetecaceg aagtagetet 60
tegactegte gaaceetgee cagetgeage aacaateget gageeceage gateeaggag 120
gateetagte acaeggeget etegactegt gegeagaget ateeagaage tegeogaga 180
tegeogetege ttaceeggag aggaateget gtteteece teeaaagate cagatetgae 240
ggatgeagea caaaceeaag ecetetteea gaaggtacag eceaceeate teateeatet 300

tgctgcaatg gtaggaggcc ttttccggaa tatcaaatac aacttggatt tctggaggaa 360 gaatgtgcac atcaatgaca acgtcctgca ctcagctttc gaggtgggca ctcgcaaggt 420 ggtctcctgc ctgtccacct gtatcttccc tgacaagacc acctatccta ttgatgaaac 480 aatgatccac aatggtccac cccacagcag caattttggg tactcgtatg ccaagaggat 540 gattgacgtg cagaacaggg cctacttcca gcagcatggc tgcaccttca ctgctgtcat 600 ccctaccaat gtctttggac ctcatgacaa cttcaacatt gaagatggcc atgtgctgcc 660 tggcctcatc cataaggtgc atctggccaa gagtaatggt tcagccttga ctgtttgggg 720 tacagggaaa ccacggaggc agttcatcta ctcactggac ctagcccggc tcttcatctg 780 ggtcctgcgg gagtacaatg aagttgagcc catcatectc tcagtgggcg aggaagatga 840 agtotocatt aaggaggcag otgaggotgt agtggaggoo atggacttot gtggggaagt 900 cacttttgat tcaacaaagt cagatgggca gtataagaag acagccagca atggcaagct 960 tegggeetae ttgeetgatt teegttteae accetteaag eaggetgtga aggagaeetg 1020 tgcctggttc accgacaact atgagcaggc ccggaagtga agcatgggac aagcgggtgc 1080 teagetggca atgeceagte agtaggetge agteteatea tttgettgte aagaactgag 1140 gacagtatec ageaacetga gecacatget ggtetetetg ceaggggget teatgeagee 1200 atccagtagg gcccatgttt gtccatcctc gggggaaggc cagaccaaca ccttgtttgt 1260 ctgcttctgc cccaacctca gtgcatccat gctggtcctg ctgtcccttg tctaga 1316

<210> 4

<211> 321

<212> PRT

. <213> Cricetulus griseus

<40	0> 4														
Met 1	Gly	Glu	Pro	Gln 5	Gly	Ser	Arg	Arg	Ile 10	Leu	Val	Thr	Gly	Gly 15	Ser
Gly	Leu	Val	Gly 20	Arg	Ala	Ile	Gln	Lys 25	Val	Va1	Ala	Ÿsp	G1y 30	Ala	Gly
Leu	Pro	Gly 35	Glu	Glu	Trp	Val	Phe 40	Val	Ser	Ser	Lys	Asp 45	Ala	Asp	Leu
Thr	Asp 50	Ala	Αla	Gln	Thr	Gln 55	·Ala	Leu	Phe	Gln	Lys 60	Val	G1n	Pro	Thr
His 65	Val	Ile	His	Leu	Ala 70	Ala	Met.	Val	Gly	.Gly 75	Leu	Phe	Arg	Asn	Ile 80
Lys	Tyr	Asn	Leu	Asp 85	Phe	Trp	Arg	Lys	Asn 90	Val	His	Ile	Asn	Asp 95	Asn
Val	Leu	His	Ser 100	Ala	Phe	Glu	Val	Gly 105	Thr	Arg	Lys	Val	Val	Ser	Cys
Leu	Ser	Thr, 115	Cys	Ile	Phe	Pro	Asp 120	Lys	Thr	Thr	Tyr	Pro 125	Ile	Asp	Glu
Thr	Met 130	Ile	His	Asn	•	Pro 135		His	Ser	Ser	Asn 140	Phe	G1y	Tyr	Ser
Tyr 145	Ala	Lys	Arg	Met	Ile 150		Val	Gln	Asn	Arg 155	Ala	Tyr	Phe	Gln	Gln 1 [.] 60
His	Gly	Cys	Thr	Phe 165	Thr	Ala	Val	Ile	Pro 170	Thr	Asn	Val	Phe	Gly 175	Pro
Иiс	l an	lan	Dhe	Agn	Tle '	'G111	Aen.	Gl v	Hic	Va 1	I.e.11	Dro	Cl v	11م.آ	Tle

180

His Lys Val His Leu Ala Lys Ser Asn Gly Ser Ala Leu Thr Val Trp 195 200 205

Gly Thr Gly Lys Pro Arg Arg Gln Phe Ile Tyr Ser Leu Asp Leu Ala 210 215 220

Arg Leu Phe Ile Trp Val Leu Arg Glu Tyr Asn Glu Val Glu Pro Ile 225 230 235 240

Ile Leu Ser Val Gly Glu Glu Asp Glu Val Ser Ile Lys Glu Ala Ala 245 250 255

Glu Ala Val Val Glu Ala Met Asp Phe Cys Gly Glu Val Thr Phe Asp 260 265 270

Ser Thr Lys Ser Asp Gly Gln Tyr Lys Lys Thr Ala Ser Asn Gly Lys 275 280 285

Leu Arg Ala Tyr Leu Pro Asp Phe Arg Phe Thr Pro Phe Lys Gln Ala 290 295 300

Val Lys Glu Thr Cys Ala Trp Phe Thr Asp Asn Tyr Glu Gln Ala Arg 305 310 315 320

Lys

<210> 5

<211> 2008

<212> DNA

<213> Cricetulus griseus

· <400> 5

aacagaaact tattttcctg tgtggctaac tagaaccaga gtacaatgtt tccaattctt 60

tgagctccga gaagacagaa gggagttgaa actctgaaaa tgcgggcatg gactggttcc 120 tggcgttgga ttatgctcat tctttttgcc tgggggacct tattgtttta tataggtggt 180 cattlggttc gagataatga ccaccctgac cattctagca gagaactctc caagattctt 240 gcaaagctgg agcgcttaaa acaacaaaat gaagacttga ggagaatggc tgagtctctc 300 cgaataccag aaggccctat tgatcagggg acagctacag gaagagtccg tgttttagaa 360 gaacagcttg ttaaggccaa agaacagatt gaaaattaca agaaacaagc taggaatgat 420 ctgggaaagg atcatgaaat cttaaggagg aggattgaaa atggagctaa agagctctgg 480 ttttttctac aaagtgaatt gaagaaatta aagaaattag aaggaaacga actccaaaga 540 catgcagatg aaattctttt ggatttagga catcatgaaa ggtctatcat gacagatcta 600 tactacctca gtcaaacaga tggagcaggt gagtggcggg aaaaagaagc caaagatctg 660 acagagetgg tecageggag aataacatat etgeagaate ceaaggaetg cageaaagee 720 agaaagctgg tatgtaatat caacaaaggc tgtggctatg gatgtcaact ccatcatgtg 780 gtttactgct tcatgattgc ttatggcacc cagcgaacac tcatcttgga atctcagaat 840 tggcgctatg ctactggagg atgggagact gtgtttagac ctgtaagtga gacatgcaca 900 gacaggtctg gcctctccac tggacactgg tcaggtgaag tgaaggacaa aaatgttcaa 960 gtggtcgagc tccccattgt agacagcctc catcctcgtc ctccttactt acccttggct 1020 gtaccagaag accttgcaga tcgactcctg agagtccatg gtgatcctgc agtgtggtgg 1080 gtateceagt ttgtcaaata ettgateegt eeacaacett ggetggaaag ggaaatagaa 1140 gaaaccacca agaagcttgg cttcaaacat ccagttattg gagtccatgt cagacgcact 1200

gacaaagtgg gaacagaagc agccttccat cccattgagg aatacatggt acacgttgaa 1260 gaacatttte agettetega acgeagaatg aaagtggata aaaaaagagt gtatetggee 1320 actgatgacc cttctttgtt aaaggaggca aagacaaagt actccaatta tgaatttatt 1380 agtgataact ctatttcttg gtcagctgga ctacacaacc gatacacaga aaattcactt 1440 cggggcgtga tcctggatat acactttctc tcccaggctg acttccttgt gtgtactttt 1500 tcatcccagg tctgtagggt tgcttatgaa atcatgcaaa cactgcatcc tgatgcctct 1560 gcaaacttcc attctttaga tgacatctac tattttggag gccaaaatgc ccacaaccag 1620 attgcagttt atcctcacca acctcgaact aaagaggaaa tccccatgga acctggagat 1680 atcattggtg tggctggaaa ccattggaat ggttactcta aaggtgtcaa cagaaaacta 1740 ggaaaaacag gcctgtaccc ttcctacaaa gtccgagaga agatagaaac agtcaaatac 1800 cctacatatc ctgaagctga aaaatagaga tggagtgtaa gagattaaca acagaattta 1860 gttcagacca tctcagccaa gcagaagacc cagactaaca tatggttcat tgacagacat 1920 gctccgcacc aagagcaagt gggaaccctc agatgctgca ctggtggaac gcctctttgt 1980 2008 gaagggctgc tgtgccctca agcccatg

<210> 6

<211> 1728

<212> DNA

<213> Mus musculus

<400> 6

atgcgggcat ggactggttc ctggcgttgg attatgctca ttctttttgc ctgggggacc 60

ttgttatttt atataggtgg tcatttggtt cgagataatg accaccctga tcactccagc 120 agagaactct ccaagattct tgcaaagctt gaacgcttaa aacagcaaaa tgaagacttg 180 aggcgaatgg ctgagtctct ccgaatacca gaaggcccca ttgaccaggg gacagctaca 240 ggaagagtcc gtgttttaga agaacagctt gttaaggcca aagaacagat tgaaaattac 300 aagaaacaag ctagaaatgg tctggggaag gatcatgaaa tcttaagaag gaggattgaa 360 aatggagcta aagagctctg gttttttcta caaagcgaac tgaagaaatt aaagcattta 420 gaaggaaatg aactccaaag acatgcagat gaaattcttt tggatttagg acaccatgaa 480 aggictatea tgacagatet atactacete agicaaacag atggagcagg ggattggcgt 540 gaaaaagagg ccaaagatct gacagagctg gtccagcgga gaataacata tctccagaat 600 cctaaggact gcagcaaagc caggaagctg gtgtgtaaca tcaataaagg ctgtggctat 660 ggttgtcaac tccatcacgt ggtctactgt ttcatgattg cttatggcac ccagcgaaca 720 ctcatcttgg aatctcagaa ttggcgctat gctactggtg gatgggagac tgtgtttaga 780 cctgtaagtg agacatgtac agacagatct ggcctctcca ctggacactg gtcaggtgaa 840 gtaaatgaca aaaacattca agtggtcgag ctccccattg tagacagcct ccatcctcgg 900 cctccttact taccactggc tgttccagaa gaccttgcag accgactcct aagagtccat 960 ggtgaccctg cagtgtggtg ggtgtcccag tttgtcaaat acttgattcg tccacaacct 1020 tggctggaaa aggaaataga agaagccacc aagaagcttg gcttcaaaca tccagttatt 1080 ggagtccatg tcagacgcac agacaaagtg ggaacagaag cagccttcca ccccatcgag 1140 gagtacatgg tacacgttga agaacatttt cagcttctcg cacgcagaat gcaagtggat 1200 aaaaaaaagag tatatctggc tactgatgat cctactttgt taaaggaggc aaagacaaag 1260
tactccaatt atgaatttat tagtgataac tctattctt ggtcagctgg actacacaat 1320
cggtacacag aaaattcact tcggggtgtg atcctggata tacactttct ctcacaggct 1380
gactttctag tgtgtacttt ttcatcccag gtctgtcggg ttgcttatga aatcatgcaa 1440
accctgcatc ctgatgcctc tgcgaacttc cattctttgg atgacatcta ctattttgga 1500
ggccaaaaatg cccacaatca gattgctgtt tatcctcaca aacctcgaac tgaagaggaa 1560
attccaatgg aacctggaga tatcattggt gtggctggaa accattggga tggttattct 1620
aaaggtatca acagaaaact tggaaaaaca ggcttatatc cctcctacaa agtccgagag 1680
aagatagaaa cagtcaagta tcccacatat cctgaagctg aaaaatag 1728

<210> 7

<211> 575

<212> PRT

<213> Cricetulus griseus

<400> 7

Met Arg Ala Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe 1 5 10 15

Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp 20 25 30

Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala 35 40 45

Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala 50 55 60

Glu Ser Leu Arg Ile Pro Glu Gly Pro Ile Asp Gln Gly Thr Ala Thr

•	00	•				. •				•	,					
	Gly	Arg	Val	Arg	Va1 85	Leu	Glu	Glu	Gln	Leu 90		Lys	Ala	Lys	Glu 95	Gln
	Ile	Glu	Asn	Tyr 100	Lys	Lys	Gln	Ala	Arg 105	Asn	Asp	Leu	Gly	Lys 110	Asp	His
	Glu	Ile	Leu 115	Arg	Arg	·Arg	Ile	Glu 120	Asn	Gly	Ala	Lys	Glu 125	Leu	Trp	Phe
	Phe	Leu 130	Gln	Ser	Glu	Leu	Lys 135		Ĺeu	Lys	Lys	Leu 140	Glu	Gly	Asn	Glu
	Leu 145	Gln	Arg	His	Ala	Asp 150	Glu	Ile	Leu	Leu	Asp 155	Leu	Gly	His	His	Glu 160
	Arg	Ser	Ile ·	Met	Thr 165	Asp	Leu	Tyr	Tyr	Leu 170	Ser	Gln	Thr	Asp	Gly 175	Ala
•	Gly	Glu	Trp	Arg 180	Glu	Lys	Glu	Ala	Lys 185		Leu	Thr	Glu	Leu 190	Val	Gln
	Arg	Arg	Ile 195	Thr	Tyr	Leu	Gln	Asn 200	Pro	Lys	Asp	Cys	Ser 205	Lys	Ala	Arg
	Lys	Leu 210	Val	Cys	Asn	Ile	Asn 215	Lys	Gly	Cys	Gly	Tyr 220	Gly	Cys	Gln	Leu
	His 225	His	Val	Val	Tyr	Cys 230	Phe	Met	Ile	Ala	Tyr 235	Gly	Thr	Gln		Thr 240
	Leu	Ile	Leu	Glu	Ser 245	Gln	Asn	Trp	Arg	Tyr 250	Ala	Thr	Gly	Gly	Trp 255	Glu

. ,14/47

Thr Val Phe Arg Pro Val Ser Glu Thr Cys Thr Asp Arg Ser Gly Leu

. 260

Ser	Thr	Gly 275		Trp	Ser	Gly	Glu 280		Lys	Asp	Lys	Asn 285		Gln	Val
Val	Glu 290	Leu	Pro	Ile	Val	Asp 295	Ser	Leu	His	Pro	Arg 300		Pro	Tyr	Leu
Pro 305	Leu	Ala	Val	Pro	Glu 310	Asp	Leu	Ala	Asp	Arg 315		Leu	Arg	Val	His 320
Gly	Asp	Pro	Ala	Val 325	Trp	Trp	Val	Ser	Gln 330	Phe	Val	Lys	Tyr	Leu 335	Ile
Arg	Pro	Gln	Pro 340	Trp	Leu	Glu	Arg	Glu 345	Ile	Glu	Glu	Thr	Thr 350	Lys	Lys
Leu	Gly.	Phe 355	Lys	His	Pro	Val	Ile 360	Gly	Val	His	Val	Arg 365	Arg	Thr	Asp
Lys	Val 370		Thr	Glu	Ala	Ala 375	Phè	His	Pro	Ile	Glu 380	Glu	Tyr	Met	Val
His 385	Val	Glu	Glu-	His	Phe 390	Gln	Leu	Leu	Glu	Arg 395	Arg	Met	Lys	Val	Asp 400
				405	Leu				410					415	٠.
· .	·		.420		Ser	•	·	425				_	430		
Ser	Trp	Ser 435	Ala	Gly	Leu	_	Asn 440	Arg	Tyr	Thr	Glu	Asn 445	Ser	Leu	Arg
	450					455					460	•			
Cys 465	Thr	Phe	Ser	Ser	Gln 470	Val	Cys	Arg		Ala 475	Tyr	Glu	Ile	•	Gln 480

Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro His Gln Pro Arg Thr Lys Glu Glu Ile Pro Met Glu Pro Gly Asp Ile Ile Gly Val Ala Gly Asn His Trp Asn Gly Tyr Ser Lys Gly Val Asn Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys <210> 8 <211> 575 <212> PRT <213> Mus musculus <400> 8 Met Arg Ala Trp Thr Gly Ser Trp Arg Trp Ile Met Leu Ile Leu Phe 10 . . Ala Trp Gly Thr Leu Leu Phe Tyr Ile Gly Gly His Leu Val Arg Asp Asn Asp His Pro Asp His Ser Ser Arg Glu Leu Ser Lys Ile Leu Ala Lys Leu Glu Arg Leu Lys Gln Gln Asn Glu Asp Leu Arg Arg Met Ala

• .	Glu 65	Ser	Leu	Arg	Ile :	Pro 70	Glu	Gly	Pro	Ile	Asp 75	Gln	Gly	Thr	Ala	Thr 80
	Gly	Arg	Val	Arg	Va1 85	Leu	Glu	Glu	Gln	Leu 90	Val	Lys	Ala	Lys	Glu 95	Gln
	Ile	Glu	Asn	Tyr 100	L y s	Lys	Gln	Ala	Arg 105	Asn	Gly	Leu	Gly	Lys 110	Asp	His
,	Glu	Ile	Leu 115	Arg	Arg	Arg	Ile	Glu 120	Asn	Gly	Ala	Lys	Glu 125	Leu	Trp	Phe
	Phe	Leu 130	Gln	Ser	Glu	Leu	Lys 135	Lys	Leu	Lys	His	Leu 140	Glu	Gly	Asn	Glu
	Leu 145	Gln	Arg	His	Ala	Asp 150	Glu	Ile	Léu	Leu	Asp 155	Leu	Gly	His	His	Glu 160
	Arg	Ser	Ile	Met	Thr 165	Asp	Leu	Tyr	Tyr	Leu 170	Ser	Gln	Thr	Asp	Gly 175	Ala
	Gly	Asp	_	Arg 180	Glu	Lys	Glu	Ala	Lys 185	Asp	Leu	Thr	Glu	Leu 1-90	Val	Gln
	Årg	Arg	Ile 195	Thr	Tyr	Leu	Gln	Asn 200	Pro	Lys	Asp	Cys	Ser 205	Lys	Ala	Arg
	Lys	Leu 210	Val	Cys	Asn	Ile	Asn 215	Lys	Gly	Cys	Gly	Tyr 220	Gly	Cys	Gln	Leu
	His 225	His	Val	Val	Tyr	Cys 230	Phe	Met	Ile	Ala	Tyr 235	Gly	Thr	Gln	Arg	Thr 240
	Leu	Ile	Leu	Glu	Ser 245	Gln	Asn	Trp	Arg	Tyr 250	Ala	Thr	Gly	Gly	Trp 255	Glu
	Thr	Val	Phe	Arg 260	Pro	Val	Ser	Glu	Thr 265	Cys	Thr	Asp	Arg	Ser 270	Gly	Leu

Ser	Thr	Gly 275	His	Trp	Ser	Gly	Glu 280	Val	Asn	Asp	Lys	Asn 285		Gln	Val
Val	Glu 290	Leu	Pro	Ile	Val	Asp 295	Ser	Leu	His	Pro	Arg 300	Pro	Pro	Tyr	Leu
Pro 305	Leu	Ala	Val	Pro	Glu 310	Asp	Leu	Ala	_	Arg 315		Leu	Arg	Val	His 320
Gly	Asp	Pro	Ala	Val 325	Trp	Trp	Val	Ser	Gln 330	Phe	Val	Lys	Tyr	Leu 335	Ile
Arg	Pṛo	Gln	Pro 340	Trp	Leu	Glu	Lys	G1u 345	Ile	Glu :	Glu ,	Ala	Thr 350	Lys	Lys
Leu	Gly	Phe 355	Lys	His	Pro	Val	Ile 360	Gly	Val	His	Val	Arg 365	Arg	Thr	Asp
Lys	Val 370		Thr	Glu	Ala	Ala 375	Phe	His	Pro	Ile	Glu 380		Tyr	Met	Val
His 385	Val	G1u	Glu	His	Phe 390	Gln.	Leu	Leu	Ala	Arg 395	Arg	Met	Gln	Val	Asp 400
Lys	Lys	Arg	Val	Tyr 405	Leu	Ala	Thr	Asp	Asp 410	Pro	Thr	Leu	Leu	Lys 415	Glu
Ala	Lys	Thr	Lys 420	Tyr	Ser	Asn	Tyr	Glu 425	Phe	Ile	Ser	Asp	Asn 430	Ser	Ilė
Ser	Trp	Ser 435	Ala	Gly	Leu	His	Asn 440	Arg	Туг	Thr		Asn 445	Ser	Leu	Arg
Gly	Val 450	Ile	Leu	Asp	Ile	His 455	Phe	Leu	Ser	Gln	Ala 460	Asp	Phe	Leu	Val

Cys Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln 465 470 475 480

Thr Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile
485
490
495

Tyr Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Val Tyr Pro
500 505 510

His Lys Pro Arg Thr Glu Glu Glu Ile Pro Met Glu Pro Gly Asp Ile 515 520 525

Ile Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Ile Asn 530 535 540

Arg Lys Leu Gly Lys Thr Gly Leu Tyr Pro Ser Tyr Lys Val Arg Glu 545 550 560

Lys Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys 565 570 575

<210> 9

<211> 383

<212> DNA

<213> Cricetulus griseus.

<400> 9

gttaactggg gctcttttaa accctgaatt tttctaaatc cccacctcca agagtttggt 60 ttaaactgat ttttttaatg aatacctttt gaagaataga gcattgtctc atcatgcaaa 120 gcttctcagg gattcagcta gcatgttgaa gaaacataag ggtgttaaat tgtttgtcac 180 aagtgctgaa taaatattga cgtagtcttc agctattcta tactggaagt agatgatatt 240 ctcattggaa attctgttag gaagtaaccc ttcttgtctt cttacctgca tagaatccca 300

ggatataaaa cttgtgcttg tcgcccttgc cattgtctct cactggtggc ctttattgca 360
tctcatatct gccttctctt tcc 383

<210> 10

<211> 504

<212> DNA

<213> Cricetulus griseus

<400> 10

taagaattcc tgtgcccagc tgtatgtgag gctctctgca ggtgtaggga tgtttctgct 60

ttctttctgc acatgcttca cagctgaagt cctttgggtg tgagattgac attcagatag 120

actaaagtga ctggacttgt tgggaaacat actgtatgca ttattgccgt tgcctccagg 180

tgaaattaac acctcattca ccaatccctg ttcatccaaa ctttctaccc acatcacttt 240

aaatagaaat tagacccaat atgactcctt ttttcctaag ctgttatag agattgtgct 300

ggagcagtga gcttttgtgt ttgtttgttt gttttgtaat tttccccatg aaaattctc 360

taaactcaaa cctaagaggg aaaaaaaaaa aacagactta tatgtgccac acttgtaaaa 420

aaaaatcatg aaagatgtat atgatattt taaacagttt gaatattaag atcacaattt 480

ctattitaaa aacaatcttg ttttacatat caatcaccca attcccttgc cttcccatcc 540

tcccattccc cccactgatc cccc 564

<400> 11-

<210> 11

<211> 120

<212> DNA

<213> Cricetulus griseus

atgaatgttc attctttggg tatatgccca agagtagaat tgctaaatat tgaggtagac 60 tgattcccat tttcttgagg agtcgccata ttgatttcca aagtgactgt acaagttaac 120

<210> 12

<211> 274

<212> DNA

<213> Cricetulus griseus

<400> 12.

aggcactagg taaatattt tgaagaaaga atgagtatct cctatttcag aaaaactttt 60 attgacttaa atttaggata tcagaattag aaaacagtaa aaatttatag gagagtttt 120 aatgaatgtt attttaaggt tccatacaaa tagtaattaa aacttacaca aactatttgt 180 agtaatgatt cagtctggta taccctgatg agcattatac acttttaaat tcttttgta 240 aatttttta ttagttcaaa ttaggaacaa gctt 274

<210> 13

<211> 9196

<212> DNA

<213> Cricetulus griseus

<400> 13

tctagaccag gctggtctcg aactcacaga gaaccacctg cctctgccac ctgagtgctg 60 ggattaaagg tgtgcaccac caccgcccgg cgtaaaatca tattttgaa tattgtgata 120 atttacatta taattgtaag taaaaatttt cagcctattt tgttatacat ttttgcgtaa 180 attattcttt tttgaaagtt ttgttgtcca taatagtcta gggaaacata aagttataat 240 ttttgtctat gtattgcat atatatctat ttaatctcct aatgtccagg aaataaatag 300

ggtatgtaat agcttcaaca tgtggtatga tagaattttt cagtgctata taagttgtta 360 cagcaaagtg ttattaattc atatgtccat atttcaattt tttatgaatt attaaattga 420 atcettaage tgecagaact agaattttat tttaateagg aageeceaaa tetgtteatt 480 ctttctatat atgtggaaag gtaggcctca ctaactgatt cttcacctgt tttagaacat 540 ggtccaagaa tggagttatg taaggggaat tacaagtgtg agaaaactcc tagaaaacaa 600 gatgagtett gtgacettag tttetttaaa aacacaaaat tettggaatg tgtttteatg 660 ttcctcccag gtggatagga gtgagtttat ttcagattat ttattacaac tggctgttgt 720 tacttgtttc tatgtcttta tagaaaaaca tattttttt gccacatgca gcttgtcctt 780 atgattttat acttgtgtga ctcttaactc tcagagtata aattgtctga tgctatgaat 840 aaagttggct attgtatgag acttcagccc acttcaatta ttggcttcat tctctcagat 900 cccaccacct ccagagtggt aaacaacttg aaccattaaa cagactttag tctttatttg 960 aatgatagat ggggatatca gatttatagg cacagggttt tgagaaaggg agaaggtaaa 1020 cagtagagtt taacaacaac aaaaagtata ctttgtaaac gtaaaactat ttattaaagt 1080 agtagacaag acattaaata ttccttggga ttagtgcttt ttgaattttg ctttcaaata 1140 atagtcagtg agtatacccc tcccccattc tatattttag cagaaatcag aataaatggt 1200 gtttctggta cattcttttg tagagaattt attttctttg ggtttttgtg catttaaagt 1260 caataaaaat taaggttcag taatagaaaa aaaactctga tttttggaat cccctttctt 1320 cagcttttct atttaatctc ttaatgataa tttaatttgt ggccatgtgg tcaaagtata 1380 tagccttgta tatgtaaatg ttttaaccaa cctgccttta cagtaactat ataattttat 1440

tctataatat atgacttttc ttccatagct ttagagttgc ccagtcactt taagttacat 1500 tttcatatat gttctttgtg ggaggagata attttatttc taagagaatc ctaagcatac 1560 tgattgagaa atggcaaaca aaacacataa ttaaagctga taaagaacga acatttggag 1620 tttaaaatac atagccaccc taagggttta actgttgtta gccttctttt ggaattttta 1680 ttagttcata tagaaaaatg gattttatcg tgacatttcc atatatgtat ataatatatt 1740 tacatcatat ccacctgtaa ttattagtgt ttttaaatat atttgaaaaa ataatggtct 1800 ggtttgatcc atttgaacct tttgatgttt ggtgtggttg ccaattggtt gatggttatg 1860 ataacctttg cttctctaag gttcaagtca gtttgagaat atgtcctcta aaaatgacag 1920 gttgcaagtt aagtagtgag atgacagcga gatggagtga tgagaatttg tagaaatgaa 1980. ttcacttata ctgagaactt gttttgcttt tagataatga acatattagc ctgaagtaca 2040 tagccgaatt gattaattat tcaaagatat aatcttttaa tccctataaa agaggtatta 2100 cacaacaatt caagaaagat agaattagac ttccagtatt ggagtgaacc atttgttatc 2160 aggtagaacc ctaacgtgtg tggttgactt aaagtgttta ctttttacct gatactgggt 2220 agctaattgt ctttcagcct cctggccaaa gataccatga aagtcaactt acgttgtatt 2280 ctatatetea aacaacteag ggtgtttett actettteea eageatgtag ageceaggaa 2340 gcacaggaca agaaagctgc ctccttgtat caccaggaag atctttttgt aagagtcatc 2400 acagtatacc agagagacta attttgtctg aagcatcatg tgttgaaaca acagaaactt 2460 attttcctgt gtggctaact agaaccagag tacaatgttt ccaattcttt gagctccgag 2520 aagacagaag ggagttgaaa ctctgaaaat gcgggcatgg actggttcct ggcgttggat 2580

tatgctcatt ctttttgcct gggggacctt attgttttat ataggtggtc atttggttcg 2640 agataatgac caccetgace attetageag agaactetee aagattettg caaagetgga 2700 gcgcttaaaa caacaaaatg aagacttgag gagaatggct gagtctctcc ggtaggtttg 2760 aaatactcaa ggatttgatg aaatactgtg cttgaccttt aggtataggg tctcagtctg 2820 ctgttgaaaa atataatttc tacaaaccgt ctttgtaaaa ttttaagtat tgtagcagac 2880 tttttaaaag tcagtgatac atctatatag tcaatatagg tttacatagt tgcaatctta 2940 ttttgcatat gaatcagtat atagaagcag tggcatttat atgcttatgt tgcatttaca 3000 attatgttta gacgaacaca aactttatgt gatttggatt agtgctcatt aaattttttt 3060 attctatgga ctacaacaga gacataaatt ttgaaaggct tagttactct taaattctta 3120 tgatgaaaag caaaaattca ttgttaaata gaacagtgca tccggaatgt gggtaattat 3180 tgccatattt ctagtctact aaaaattgtg gcataactgt tcaaagtcat cagttgtttg 3240 gaaagccaaa gtctgattta aatggaaaac ataaacaatg atatctattt ctagatacct 3300 ttaacttgca gttactgagt ttacaagttg tctgacaact ttggattctc ttacttcata 3360 tctaagaatg atcatgtgta cagtgcttac tgtcacttta aaaaactgca gggctagaca 3420 tgcagatatg aagactttga cattagatgt ggtaattggc actaccagca agtggtatta 3480 agatacaget gaatatatta etttttgagg aacataatte atgaatggaa agtggageat 3540 tagagaggat gccttctggc tctcccacac cactgtttgc atccattgca tttcacactg 3600 cttttagaac tcagatgttt catatggtat attgtgtaac tcaccatcag ttttatcttt 3660 aaatgtctat ggatgataat gttgtatgtt aacactttta caaaaacaaa tgaagccata 3720

tcctcggtgt gagttgtgat ggtggtaatt gtcacaatag gattattcag caaggaacta 3780 agtcagggac aagaagtggg cgatactttg ttggattaaa tcattttact ggaagttcat 3840 cagggagggt tatgaaagtt gtggtctttg aactgaaatt atatgtgatt cattattctt 3900 gatttaggcc ttgctaatag taactatcat ttattgggaa tttgtcatat gtgccaattt 3960 gtcatgggcc agacagcgtg ttttactgaa tttctagata tctttatgag attctagtac 4020 tgttttcagc cattttacag atgaagaatc ttaaaaaaatg ttaaataatt tagtttgccc 4080 aagattatac gttaacaaat ggtagaacct tetttgaatt etggeagtat ggetacacag 4140 tecgaactet tatetteeta agetgaaaac agaaaaagea atgacecaga aaattttatt 4200 taaaagtoto aggagagact toccatootg agaagatoto ttttcccttt tataatttag 4260 gctcctgaat aatcactgaa ttttctccat gttccatcta tagtactgtt atttctgttt 4320 tccttttttc ttaccacaaa gtatcttgtt tttgctgtat gaaagaaaat gtgttattgt 4380 aatgtgaaat tetetgteee tgeagggtee cacateegee teaateeeaa ataaacacae 4440 agaggetgta ttaattatga aactgttggt cagttggeta gggettetta ttggetaget 4500 ctgtcttaat tattaaacca taactactat tgtaagtatt tccatgtggt cttatcttac 4560 caaggaaagg gtccagggac ctcttactcc tctggcgtgt tggcagtgaa gaggagaga 4620 cgatttccta tttgtctctg cttattttct gattctgctc agctatgtca cttcctgcct 4680 ggccaatcag ccaatcagtg ttttattcat tagccaataa aagaaacatt tacacagaag 4740 gacttccccc atcatgttat ttgtatgagt tcttcagaaa atcatagtat cttttaatac 4800 taatttttat aaaaaattaa ttgtattgaa aattatgtgt atatgtgtct gtgtgtcgat 4860

ttgtgctcat aagtagcatg gagtgcagaa gagggaatca gatcttttt taagggacaa 4920 agagtttatt cagattacat tttaaggtga taatgtatga ttgcaaggtt atcaacatgg 4980 cagaaatgtg aagaagctgg tcacattaca tccagagtca agagtagaga gcaatgaatt 5040 gatgcatgca ttcctgtgct cagctcactt ttcctggagc tgagctgatt gtaagccatc 5100 tgatgtcttt gctgggaact aactcaaagg caagttcaaa acctgttctt aagtataagc 5160 catctctcca gtccctcata tggtctctta agacactttc tttatattct tgtacataga 5220 aattgaattc ctaacaactg cattcaaatt acaaaatagt ttttaaaaagc tgatataata 5280 aatgtaaata caatctagaa catttttata aataagcata ttaactcagt aaaaataaat 5340 gcatggttat tttccttcat tagggaagta tgtctcccca ggctgttctc tagattctac 5400 tagtaatgct gtttgtacac catccacagg ggttttattt taaagctaag acatgaatga 5460 tggacatgct tgttagcatt tagacttttt tccttactat aattgagcta gtatttttgt 5520 gctcagtttg atatctgtta attcagataa atgtaatagt aggtaatttc tttgtgataa 5580 aggcatataa attgaagttg gaaaacaaaa gcctgaaatg acagttttta agattcagaa 5640 caataatttt caaaagcagt tacccaactt tccaaataca atctgcagtt ttcttgatat 5700 gtgataaatt tagacaaaga aatagcacat tttaaaaatag ctatttactc ttgatttttt 5760 tttcaaattt aggctagttc actagttgtg tgtaaggtta tggctgcaaa catctttgac 5820 tcttggttag ggaatccagg atgatttacg tgtttggcca aaatcttgtt ccattctggg 5880 tttcttctct atctaggtag ctagcacaag ttaaaggtgt ggtagtattg gaaggctctc 5940 aggtatatat ttctatattc tgtatttttt tcctctgtca tatatttgct ttctgtttta 6000

ttgatttcta ctgttagttt gatacttact ttcttacact ttctttggga tttattttgc 6060 tgttctaaga tttcttagca agttcatatc actgatttta acagttgctt cttttgtaat 6120 atagactgaa tgccccttat ttgaaatgct tgggatcaga aactcagatt tgaacttttc 6180 ttttttaata tttccatcaa gtttaccagc tgaatgtcct gatccaagaa tatgaaatct 6240 gaaatgettt gaaatetgaa aettttagag tgataaaget teeetttaaa ttaatttgtg 6300 ttctatattt tttgacaatg tcaacctttc attgttatcc aatgagtgaa catattttca 6360 atttttttgt ttgatctgtt atattttgat ctgaccatat ttataaaaatt ttatttaatt 6420 tgaatgttgt getgttaett atetttatta ttatttttge ttatttteta gecaaatgaa 6480 attatattct gtattatttt agtttgaatt ttactttgtg gcttagtaac tgccttttgt 6540 tggtgaatgc ttaagaaaaa cgtgtggtct actgatattg gttctaatct tatatagcat 6600 gttgtttgtt aggtagttga ttatgctggt cagattgtct tgagtttatg caaatgtaaa 6660 atatttagat gcttgttttg ttgtctaaga acaaagtatg cttgetgtct cctatcggtt 6720 ctggtttttc cattcatctc ttcaagctgt tttgtgtgtt gaatactaac tccgtactat 6780 cttgttttct gtgaattaac cccttttcaa aggtttcttt tcttttttt tttaagggac 6840 aacaagttta ttcagattac attttaagct gataatgtat gattgcaagg ttatcaacat 6900 ggcagaaatg tgaagaagct aggcacatta catccacatg gagtcaagag cagagagcag 6960 tgaattaatg catgcattcc tgtggtcagc tcacttttcc tattcttaga tagtctagga 7020 tcataaacct ggggaatagt gctaccacaa tgggcatatc cacttacttc agttcatgca 7080 atcaaccaag gcacatccac aggaaaaact gatttagaca acctctcatt gagactcttc 7140

ccagatgatt agactgtgtc aagttgacaa ttaaaactat cacacctgaa gceatcacta 7200 gtaaatataa tgaaaatgtt gattatcacc ataattcatc tgtatccctt tgttattgta 7260 gattttgtga agttcctatt caagtccctg ttccttcctt aaaaacctgt tttttagtta 7320 aataggtttt ttagtgttcc tgtctgtaaa tactttttta aagttagata ttattttcaa 7380 gtatgttctc ccagtctttg gcttgtattt tcatcccttc aatacatata tttttgtaat 7440 ttattttttt tatttaaatt agaaacaaag ctgcttttac atgtcagtct cagttccctc 7500 teceteceet ceteceetge tececaceta agececaatt ceaacteett tetteteece 7560 aggaagggtg aggccctcca tgggggaaat cttcaatgtc tgtcatatca tttggagcag 7620 ggcctagacc ctccccagtg tgtctaggct gagagagtat ccctctatgt ggagagggct 7680 cccaaagttc atttgtgtac taggggtaaa tactgatcca ctatcagtgg ccccatagat 7740 tgtccggacc tccaaactga cttcctcctt cagggagtct ggaacagttc tatgctggtt 7800 tcccagatat cagtctgggg tccatgagca accccttgtt caggtcagtt gtttctgtag 7860 gtttccccag cccggtcttg acccctttgc tcatcacttc tccctctctg caactggatt 7920 ccagagttca geteagtgtt tagetgtggg tgtetgeate tgetteeate agetaetgga 7980 tgagggctct aggatggcat ataaggtagt catcagtctc attatcagag aagggctttt 8040 aaggtageet ettgattatt gettagattg ttagttgggg teaacettgt aggtetetgg 8100 acagtgacag aattetettt aaacetataa tggeteecte tgtggtggta teeetttet 8160 tgeteteate egiteeteec etgactagat etteetgete eeteatgiee teeteteece 8220 teceettete ceettetett tettetaact eeeteteee tecaeceaeg ateceeatta 8280

gettatgaga tettgteett attttageaa aacetttttg getataaaat taattaattt 8340 aatatgetta tateaggttt attttggeta gtatttgtat gtgtttggtt agtgttttta 8400 accttaattg acatgtatcc ttatatttag acacagattt aaatatttga agtttttttt 8460 ttttttttt ttaaagattt atttatttt tatgtettet geetgeatge cagaagaggg 8520 caccagatet catteaaggt ggttgtgage caccatgtgg ttgetgggaa ttgaacteag 8580 gacctetgga agaacagtea gtgetettaa eegetgagee ateteteeag eecetgaagt 8640 gtttctttta aagaggatag cagtgcatca tttttccctt tgaccaatga ctcctacctt 8700 actgaattgt tttagccatt tatatgtaat gctgttacca ggtttacatt ttctttatc 8760 ttgctaaatt tcttccctgt ttgtctcatc tcttattttt gtctgttgga ttatataggc 8820 ttttattttt ctgtttttac agtaagttat atcaaattaa aattatttta tggaatgggt 8880 gtgttgacta catgtatgtc tgtgcaccat gtgctgacct ggtcttggcc agaagaaggt 8940 gtcatattct ctgaaactgg tattgtggat gttacgaact gccatagggt gctaggaatc 9000 aaaccccage teetetggaa aagcageeae tgetetgage caetgagtee tetetteaag 9060 caggtgatgc caacttttaa tggttaccag tggataagag tgcttgtatc tctagcaccc 9120 atgaaaattt atgcattgct atatgggctt gtcacttcag cattgtgtga cagagacagg 9180 9196 aggateceaa gagete

<210> 14

<211> 5

<212> PRT

<213> Mus musculus

```
<400> 14
Asn Tyr Asn Met Asp
  1
<210> 15
<211> 17
<212> PRT
<213> Mus musculus
<400> 15
Tyr Ile Tyr Pro Asn Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe Lys
  1
                                      10
                                                           15
Ser
<210> 16
<211> 11
<212> PRT
<213> Mus musculus
<400> 16.
Thr Gly His Tyr Tyr Gly Tyr Met Phe Ala Tyr
. 1
                  5
                                      10
<210> 17⋅
<211> 10
<212> PRT
<213> Mus musculus
<400> 17
Ser Ala Ser Ser Ser Val Ser Tyr Met His
```

10

1

5

```
⟨210⟩ 18
<211> 7
<212> PRT
<213> Mus musculus
<400> 18
Ser Thr Ser Asn Leu Ala Ser
 . 1
                  5.
<210> 19
<211> 9
<212> PRT
<213> Mus musculus
<400> 19
Gln Gln Arg Ser Ser Tyr Pro Tyr Thr
                  5
<210> 20
<211> 120
<212> PRT
<213> Mus musculus
Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
  1
                  5
                                                           15
                                      10 .
Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
             20
                                  25
                                                       30
Asn Met Asp Trp Val Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile
         35
                              40
                                                   45
Gly Tyr Ile Tyr Pro Asn Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe
                                              60
     50
                          55
```

Lys Ser Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr Met Glu Leu His Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Thr Tyr Gly His Tyr Tyr Gly Tyr Met Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala <210> 21 <211> 107 <212> PRT <213> Mus musculus <400> 21 Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu . 75 Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Tyr Thr

100 105 <210> 22 <211> 125 <212> PRT <213> Artificial sequence <220> <223> Description of Artificial Sequence: Amino Acid Sequence of Antibody Heavy Chain Variable Region <400> 22 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala 5 1 10 15 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr 25 Asn Met Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met 35 40 45 Gly Tyr Ile Tyr Pro Asn Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe 50 60. Lys Ser Lys Val Thr Ile Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr 65 70 75 80 Met Glu Leu His Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95 Ala Thr Tyr Gly His Tyr Tyr Gly Tyr Met Phe Ala Tyr Trp Gly Gln 100 105 110 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly 120 125 115

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg

<210> 23 <211> 125 . <212> PRT <213> Artificial Sequence ⟨220⟩ <223> Description of Artificial Sequence: Amino Acid Sequence of Antibody Heavy Chain Variable Region <400> 23 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala 1 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr 50 65

Asn Met Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met 35 40 45 Gly Tyr Ile Tyr Pro Asn Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe 55 60 Lys Ser Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala Tyr 70 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 Ala Arg Tyr Gly His Tyr Tyr Gly Tyr Met Phe Ala Tyr Trp Gly Gln 100 105

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly

120

5

20

<210> 24 <211> 108

. 115

10

15

80

95

110

125

30

<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artif
Chain Variable Region
<400> 24
Asp Ile Gln Leu Thr Gln Set
1 5
Asp Arg Val Thr Ile Thr Cy
20

<223> Description of Artificial Sequence: Amino Acid Sequence of Antibody Light Chain Variable Region

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr 35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser 50 55 60

Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu 65 70 75 80

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Tyr Thr 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr
100 105

<210> 25

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino Acid Sequence of Antibody Light Chain Variable Region

<400> 25 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly 10 1 5 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met 20 25 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr 40 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser 60 55 50 Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu 75 65 70 80 Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Tyr Thr 85 Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr 100 105 <210> 26 <211> 125 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Amino Acid Sequence of Antibody Heavy Chain Variable Region <400> 26 Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala 1 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr

Asn Met Asp Trp Val Lys Gln Ser Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

25

Gly Tyr Ile Tyr Pro Asn Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe
50 55 60

Lys Ser Lys Val Thr Ile Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr 65 70 75 80

Met Glu Leu His Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95

Ala Thr Tyr Gly His Tyr Tyr Gly Tyr Met Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

<210> 27

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino Acid Sequence of Antibody Heavy Chain Variable Region

<400> 27

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr 20 25 30

Asn Met Asp Trp Val Lys Gln Ser Pro Gly Lys Ser Leu Glu Trp Met

Gly Tyr Ile Tyr Pro Asn Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe 50 55 60

40

Lys Ser Lys Val Thr Ile Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr 65 70 75 80

Met Glu Leu His Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95

Ala Thr Tyr Gly His Tyr Tyr Gly Tyr Met Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

<210> 28

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino Acid Sequence of Antibody Heavy Chain Variable Region

<400> 28

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr 20 25 30

Asn Met Asp Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met 35 40 45

Gly Tyr Ile Tyr Pro Asn Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe

Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr 65 70 75 80

Met Glu Leu His Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95

Ala Thr Tyr Gly His Tyr Tyr Gly Tyr Met Phe Ala Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

<210> 29

<211> 125

<212> PRT

<213> Artificial Sequence

(220)

<223> Description of Artificial Sequence: Amino Acid Sequence of Antibody Heavy Chain Variable Region

<400> 29

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr 20 . 25 30

Asn Met Asp Trp Val Lys Gln Ser Pro Gly Lys Ser Leu Glu Trp Met
35 40 45

Gly Tyr Ile Tyr Pro Asn Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe 50 55 60

Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr

Met Glu Leu His Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys 85 90 95

Ala Thr Tyr Gly His Tyr Tyr Gly Tyr Met Phe Ala Tyr Trp Gly Gln 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly 115 120 125

70.

<210> 30

<211> 125

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino Acid Sequence of Antibody Heavy Chain Variable Region

· <400> 30

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala 1 5 10

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr 20 . 25 30

Asn Met Asp Trp Val Lys Gln Ser Pro Gly Gln Gly Leu Glu Trp Met 35 40 ' 45

Gly Tyr Ile Tyr Pro Asn Asn Gly Gly Thr Gly Tyr Asn Gln Lys Phe 60 50 55

Lys Ser Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Ser Thr Ala Tyr 65 70 80

Met Glu Leu His Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

90

95

Ala Thr Tyr Gly His Tyr Tyr Gly Tyr Met Phe Ala Tyr Trp Gly Gln ' 105 -110 100 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly 115 120 125 <210> 31 <211> 108 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Amino Acid Sequence of Antibody Light Chain Variable Region <400> 31 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Pro Gly 1 5 10 15 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met 20 · 25 30 His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr 35 40 45 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser 50 55 60 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Leu Gln Pro Glu 65 80 70 75

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr

85

90

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Tyr Thr

<210> 32

⟨211⟩ 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino Acid Sequence of Antibody Light Chain Variable Region

<400> 32

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Pro Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met 20 25 30

His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr 35 40 45

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser 50 55 60 7

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Leu Gln Pro Glu 65 70 75 80

Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Tyr Thr 85 90 95

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr 100 105

<210> 33

<211> 108

<212> PRT

<213> Artificial Sequence <220> <223> Description of Artificial Sequence: Amino Acid Sequence of Antibody Light Chain Variable Region <400> 33 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Pro Gly 5 · 10 15 1 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met 25 30 20 His Trp Phe Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr 35 40 · 45 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser 50 55 Gly Ser Gly Thr Ser Tyr Ser Phe Thr Ile Ser Ser Leu Gln Pro Glu 80 65 70 Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Tyr Thr 95 90 85 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr

100 105

<210> 34

<211> 108

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino Acid Sequence of Antibody Light Chain Variable Region

<400> 34 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Pro Gly 15 5 10 1 Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met 25 20 His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr 45 40 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser 60 55 50 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Leu Gln Pro Glu 80 70 · 65 Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Tyr Thr 95 90 85 Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg Thr 100 105 <210> 35 <211> 108 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Amino Acid Sequence of Antibody Light Chain Variable Region <400> 35 Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Met Ser Ala Ser Pro Gly 15 10 1

Asp Arg Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met 25 30 20 His Trp Phe Gln Gln Lys Pro Gly Lys Ser Pro Lys Leu Trp Ile Tyr 45 40 35 Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser 60 55 50 Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Gln Pro Glu 75 65 70 Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Tyr Thr 90 85 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr 100 105 <210> 36 <211> 28 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic DNA <400> 36 28 gagacttcag cccacttcaa ttattggc <210> 37 <211> 25 <212> DNA <213> Artificial Sequence <220>

<223> Description of Artificial Sequence: Synthetic DNA

```
" <400% 37
cttgtgtgac tcttaactct cagag
```

25

<210> 38

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 38

gaggccactt gtgtagcgcc aagtg

25

⟨210⟩ 39

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA

<400> 39

ccctcgagat aacttcgtat agc

23

<210> 40

<211> 18°

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence : Synthetic DNA

<400> 40

<210> 41	
<211> 25	
<212> DNA .	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence : Synthetic DNA	
<400> 41	
catagaaaca agtaacaaca gccag	25
	ω.
<210> 42	
<211> 21	
<212> DNA	
<213> Artificial Sequence	
⟨220⟩	
<223> Description of Artificial Sequence: Synthetic DNA	
value begeinputed of Artificial bequence. Symmetre bux	
<400> 42	
gtgagtccat ggctgtcact g	21
<210> 43	٠
<211> 20	
<212> DNA <213> Artificial Sequence	
varo, wrotitorar podacinos	
<220>	
<223> Description of Artificial Sequence: Synthetic DNA	
<400> 43	
cctgacttgg ctattctcag	20

This Page is Inserted by IFW Indexing and Scanning Operations and is not part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

☐ BLACK BORDERS
☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
☐ FADED TEXT OR DRAWING
BLURRED OR ILLEGIBLE TEXT OR DRAWING
☐ SKEWED/SLANTED IMAGES
☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
☐ GRAY SCALE DOCUMENTS
LINES OR MARKS ON ORIGINAL DOCUMENT
REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
□ other:

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.